

[illegible]

DB	545	agcctagagctcaactcccaaatctgctcttaadactgacacgcttgaatccagaggaagct	604
QY	601	ttctggaattcccaqtgtaagatcgaattcgaattataggaagaacacgaatgacga	660
DB	605	gaatgaattcccaqtgtaagatcgaattcgaattataggaagaacacgaatgacga	664
QY	661	agcaggaacacgaatgataatgaatgagctgagcgaagagatgaggaagaacacgaat	720
DB	665	agcaggaacacgaatgataatgaatgagctgagcgaagagatgaggaagaacacgaat	724
QY	721	taataacctggaattcccaqtgtaagatcgaattcgaattataggaagaacacgaat	780
DB	725	taataacctggaattcccaqtgtaagatcgaattcgaattataggaagaacacgaat	784
QY	781	ctcagtgctgagctgagcgaacacgaatgaggaagaacacgaatgaggaagaacacgaat	840
DB	785	ctcagtgctgagctgagcgaacacgaatgaggaagaacacgaatgaggaagaacacgaat	844
QY	841	actcaggaacacgaatgagcgaacacgaatgaggaagaacacgaatgaggaagaacacgaat	900
DB	845	actcaggaacacgaatgagcgaacacgaatgaggaagaacacgaatgaggaagaacacgaat	904
QY	901	acgcaggaacacgaatgagcgaacacgaatgaggaagaacacgaatgaggaagaacacgaat	960
DB	905	acgcaggaacacgaatgagcgaacacgaatgaggaagaacacgaatgaggaagaacacgaat	964
QY	961	acgcaggaacacgaatgagcgaacacgaatgaggaagaacacgaatgaggaagaacacgaat	1020
DB	965	acgcaggaacacgaatgagcgaacacgaatgaggaagaacacgaatgaggaagaacacgaat	1024
QY	1021	agcctagagctcaactcccaaatctgctcttaadactgacacgcttgaatccagaggaagct	1080
DB	1025	agcctagagctcaactcccaaatctgctcttaadactgacacgcttgaatccagaggaagct	1084
QY	1081	actctagagaacacgaatgagcgaacacgaatgaggaagaacacgaatgaggaagaacacgaat	1140
DB	1085	actctagagaacacgaatgagcgaacacgaatgaggaagaacacgaatgaggaagaacacgaat	1144
QY	1141	agcctctatctcagcgaacacgaatgaggaagaacacgaatgaggaagaacacgaatgaggaagaacacgaat	1200
DB	1145	agcctctatctcagcgaacacgaatgaggaagaacacgaatgaggaagaacacgaatgaggaagaacacgaat	1204
QY	1201	atgacatcagcgaacacgaatgaggaagaacacgaatgaggaagaacacgaatgaggaagaacacgaat	1260
DB	1205	atgacatcagcgaacacgaatgaggaagaacacgaatgaggaagaacacgaatgaggaagaacacgaat	1264
QY	1261	acatagaggaacacgaatgaggaagaacacgaatgaggaagaacacgaatgaggaagaacacgaat	1320
DB	1265	acatagaggaacacgaatgaggaagaacacgaatgaggaagaacacgaatgaggaagaacacgaat	1324
QY	1321	gactctatcagcgaacacgaatgaggaagaacacgaatgaggaagaacacgaatgaggaagaacacgaat	1380
DB	1325	gactctatcagcgaacacgaatgaggaagaacacgaatgaggaagaacacgaatgaggaagaacacgaat	1384
QY	1381	acgcaggaacacgaatgaggaagaacacgaatgaggaagaacacgaatgaggaagaacacgaat	1440
DB	1385	acgcaggaacacgaatgaggaagaacacgaatgaggaagaacacgaatgaggaagaacacgaat	1444

Figure 1

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Detailed description of Figure 1: This is a Western blot image showing protein levels in C2C12 myoblasts. The blot is divided into four vertical lanes. The first lane is labeled 'Control'. The second lane is labeled '100 ng/ml TNF-α'. The third lane is labeled '100 ng/ml TNF-α + 100 ng/ml SB203580'. The fourth lane is labeled '100 ng/ml TNF-α + 100 ng/ml SB203580 + 100 ng/ml LY294002'. On the left side of the blot, there are molecular weight markers in kilodaltons (kDa): 43, 36, 29, 21, 14, and 12. Three specific protein bands are identified: 'p38' at approximately 38 kDa, 'p38 phosphorylated' at approximately 38 kDa (appearing as a slightly higher band), and 'GAPDH' at approximately 36 kDa. The p38 and p38 phosphorylated bands show a significant increase in intensity in the TNF-α treated lane compared to the control, which is partially inhibited by SB203580 and further by the combination with LY294002. The GAPDH band, used as a loading control, shows consistent intensity across all four lanes.

1. *Chlorophyll a* (Chl *a*)
 2. *Chlorophyll b* (Chl *b*)
 3. *Chlorophyll c* (Chl *c*)
 4. *Chlorophyll d* (Chl *d*)
 5. *Chlorophyll e* (Chl *e*)
 6. *Chlorophyll f* (Chl *f*)
 7. *Chlorophyll g* (Chl *g*)
 8. *Chlorophyll h* (Chl *h*)
 9. *Chlorophyll i* (Chl *i*)
 10. *Chlorophyll j* (Chl *j*)
 11. *Chlorophyll k* (Chl *k*)
 12. *Chlorophyll l* (Chl *l*)
 13. *Chlorophyll m* (Chl *m*)
 14. *Chlorophyll n* (Chl *n*)
 15. *Chlorophyll o* (Chl *o*)
 16. *Chlorophyll p* (Chl *p*)
 17. *Chlorophyll q* (Chl *q*)
 18. *Chlorophyll r* (Chl *r*)
 19. *Chlorophyll s* (Chl *s*)
 20. *Chlorophyll t* (Chl *t*)
 21. *Chlorophyll u* (Chl *u*)
 22. *Chlorophyll v* (Chl *v*)
 23. *Chlorophyll w* (Chl *w*)
 24. *Chlorophyll x* (Chl *x*)
 25. *Chlorophyll y* (Chl *y*)
 26. *Chlorophyll z* (Chl *z*)
 27. *Chlorophyll aa* (Chl *aa*)
 28. *Chlorophyll ab* (Chl *ab*)
 29. *Chlorophyll ac* (Chl *ac*)
 30. *Chlorophyll ad* (Chl *ad*)
 31. *Chlorophyll ae* (Chl *ae*)
 32. *Chlorophyll af* (Chl *af*)
 33. *Chlorophyll ag* (Chl *ag*)
 34. *Chlorophyll ah* (Chl *ah*)
 35. *Chlorophyll ai* (Chl *ai*)
 36. *Chlorophyll aj* (Chl *aj*)
 37. *Chlorophyll ak* (Chl *ak*)
 38. *Chlorophyll al* (Chl *al*)
 39. *Chlorophyll am* (Chl *am*)
 40. *Chlorophyll an* (Chl *an*)
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 129. *Chlorophyll a77* (Chl *a77*)
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Variable	Mean	SD	Min	Max
Age	34.5	10.2	21	55
Gender	0.45	0.50	0	1
Marital status	0.60	0.49	0	1
Education	12.5	1.5	9	16
Income	1500	500	500	3000
Health status	0.70	0.46	0	1
Employment	0.80	0.42	0	1
Life satisfaction	4.5	1.2	1	7
Depression	0.30	0.46	0	1
Stress	3.5	1.5	1	7
Resilience	5.0	1.0	3	7
Optimism	5.5	1.0	3	7
Gratitude	5.0	1.0	3	7
Forgiveness	5.0	1.0	3	7
Self-esteem	5.0	1.0	3	7
Life purpose	5.0	1.0	3	7
Meaning in life	5.0	1.0	3	7
Existential well-being	5.0	1.0	3	7
Overall well-being	5.0	1.0	3	7

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 90. **Notes**
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 92. **Appendix**
 93. **Notes**
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 95. **Appendix**
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 99. **Notes**
 100. **References**

[illegible]

Figure 1

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[illegible]

Figure 1. Schematic representation of the experimental design. The subjects were divided into two groups: the control group (CG) and the experimental group (EG). The CG was divided into two subgroups: the control group (CG) and the control group (CG). The EG was divided into two subgroups: the experimental group (EG) and the experimental group (EG). The subjects were divided into two groups: the control group (CG) and the experimental group (EG). The CG was divided into two subgroups: the control group (CG) and the control group (CG). The EG was divided into two subgroups: the experimental group (EG) and the experimental group (EG).

[illegible]

The diagram illustrates the experimental setup. A subject is seated at a table, looking at a video screen. A camera is positioned above the screen. A target is placed on the table. A horizontal arrow indicates the direction of movement from the starting point to the target. A vertical arrow indicates the direction of movement from the starting point to the video screen. A horizontal arrow indicates the direction of movement from the video screen to the target. A vertical arrow indicates the direction of movement from the video screen to the camera.

100
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 0 10 20 30 40 50 60 70 80 90 100

Figure 1: Schematic representation of the experimental design. The diagram illustrates the flow of information in the experiment. It starts with a 'Stimulus' (a word) being presented to a 'Subject'. The 'Subject' provides a 'Response' (a word), which is then processed by a 'Computer'. The 'Computer' outputs a 'Response' (a word), which is then presented to the 'Subject'. The 'Subject's' response is then processed by the 'Computer', which outputs a final 'Response' (a word). The diagram is labeled 'Figure 1' and 'Schematic representation of the experimental design'.

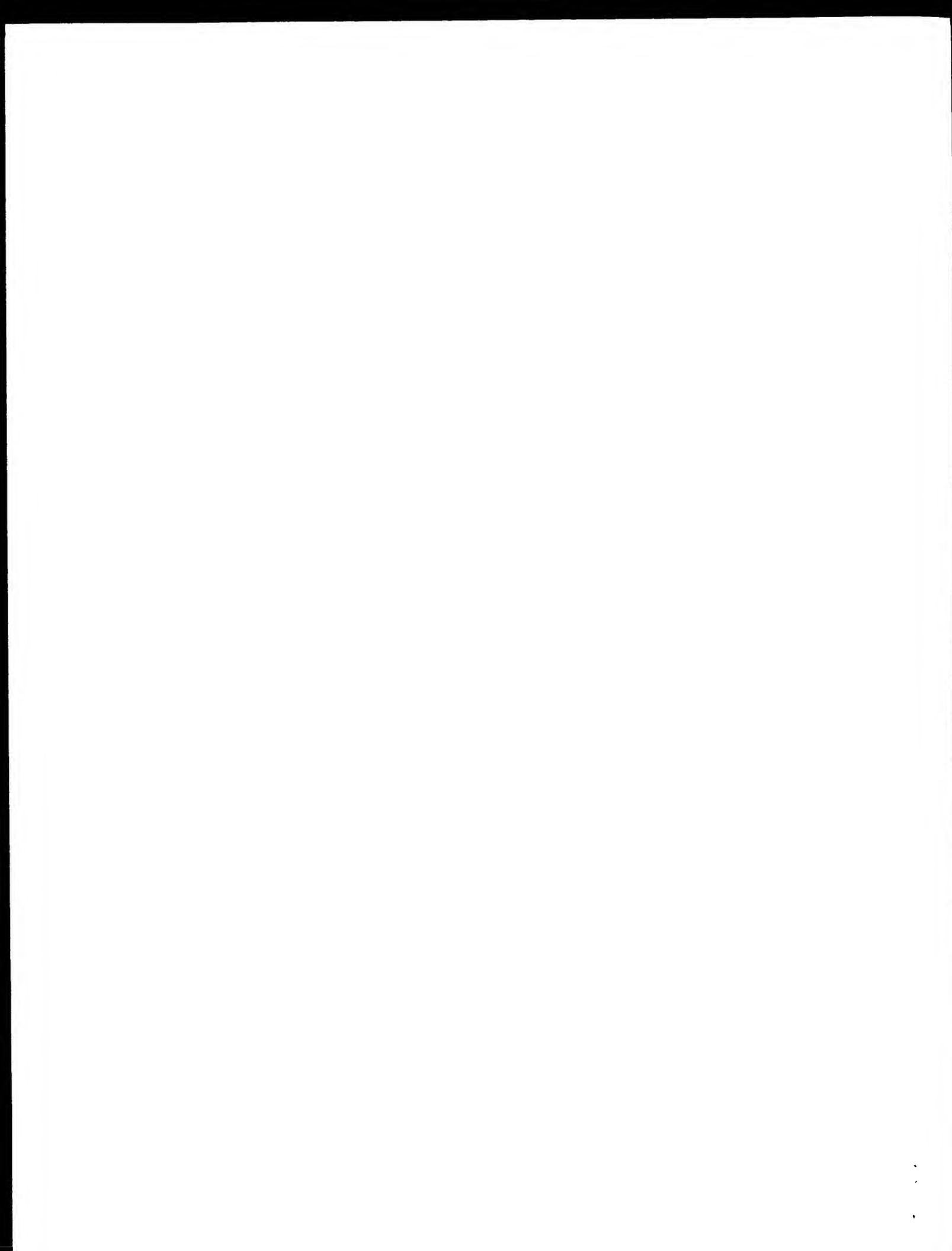
[illegible]

Figure 1 is a schematic representation of the experimental design. It shows a vertical flow of steps: 1. Selection of 1000 subjects, 2. Random assignment to two groups (500 each), 3. Pre-test (1000 subjects), 4. Training (500 subjects), 5. Post-test (500 subjects), 6. Follow-up (500 subjects), 7. Final test (500 subjects).

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27 1561 1420
 11 1543 1403
 25 1521 1380
 14 1501 1360
 25 1481 1325
 11 1461 1285
 27 1441 1245
 11 1421 1205
 27 1401 1165
 11 1381 1125
 27 1361 1085
 11 1341 1045
 27 1321 1005
 11 1301 965
 27 1281 925
 11 1261 885
 27 1241 845
 11 1221 805
 27 1201 765
 11 1181 725
 27 1161 685
 11 1141 645
 27 1121 605
 11 1101 565
 27 1081 525
 11 1061 485
 27 1041 445
 11 1021 405
 27 1001 365
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 27 921 205
 11 901 165
 27 881 125
 11 861 85
 27 841 45
 11 821 5
 27 801 0
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 11 181 0
 27 161 0
 11 141 0
 27 121 0
 11 101 0
 27 81 0
 11 61 0
 27 41 0
 11 21 0
 27 1 0

Best Local Similarity 66.6%; Prod. No. 1.4e-274;
 Matches 950; Conservative 224; Mismatches 225; Indels 28; Gaps 6;
 07 12 71
 1b 60
 07 72 15
 1b 120
 07 19
 1b 178
 07 251
 1b 258
 07 311
 1b 298
 07 372
 1b 418
 07 432
 1b 478
 07 551
 1b 538
 07 599
 1b 611
 07 658
 1b 718
 07 791
 1b 777
 07 851
 1b 857
 07 911
 1b 907
 07 971
 1b 956
 07 1043
 1b 1015
 07 1042
 1b 1041




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1188 -----GTTAATCCCAAGACCATCTCATTGGGATTTCCTTCTGCACACTCGAAG 1238
1261 acatgaaggtacatacctaatcccaattacacactgcacacgtaaacatccccc 1320
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1298 GATCAAGATTGAATCGGTAGTAATCGTGGAACACGATGCGGTGTCGAAATACCT 1297
1321 accttctaccacacacgcgcgtcacacacatgggaatttttcttaccacaaacccct 1380
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1298 GGCTTGATACACACCGCGCGGTACACCAATGCGAGTGGTTCCTATACCGAACAGN 1457
1381 acccgaaagacacacacacacacacacacacacacacacacacacacacacac 1438
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1358 ACCTTCGGGGGCGACGCGGCCACGATAGATCACAGACTGCGGCGAAGTGGTAACA 1415

RESULT          6
US-08-518A-1
Sequence 1, Application no. 0800518A
Patent No. 593508
GENERAL INFORMATION:
APPLICANT: Joseph Hirschberg and Mark Barker
TITLE OF INVENTION: NOVEL CAROTENOIDS-PRODUCING BACTERIAL
TITLE OF INVENTION: SPECIES AND PROCESS FOR PRODUCTION
TITLE OF INVENTION: OF CAROTENOIDS USING SAME
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSER: Mark M. Friedman c/o Robert Steinbohn
STREET: 2940 Birchtree lane
CITY: Silver Spring
STATE: Maryland
COUNTRY: United States of America
ZIP: 20906
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.14 megabyte, 3.5" microdisk
COMPUTER: Twhinhead* Stimote-890TX
OPERATING SYSTEM: MS DOS version 6.2
OPERATING SYSTEM: Windows version 3.11
SOFTWARE: Word for Windows version 2.0 converted to
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/902.518A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Friedman, Mark M.
REGISTRATION NUMBER: 43,884
REFERENCE/DOCID NUMBER: 325/20
TELECOMMUNICATION INFORMATION:
TELEPHONE: 972-3-562553
TELEFAX: 972-3-562554
TIPTX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1430
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: Linear
IS-08-902-518A-1

```

QUESTIONS

Best. local Similarity 66.6%; Pred. No. 1.5e-300;

Matches 950; Conservative 224; Mismatches 225; Models 28;

10. *Journal of the American Statistical Association*, 71

10

1 CAGAACGAAACCGUCCGGCAGGCUUAAACAACAUACAAGUCGACCGAGACCUUUGGUCUAG 60

US-08-632-470-28

Query Match 64.9%; Score 941 4; Pos 2; Length 1440;
Best Local Similarity 80.7%; Pred. No. 5,6e 294;
Matches 1147; Mismatches 6; Mismatch-bases 257; Indels 22; Gaps 6;

QY 5 cctaggtcdaagcgaacatgagcagatgcttaacacatgcaagtcgcaagcatttcc 64
DB 1 cctggtctcagaaagcaagcgtatcggtatgcttaacacatgcaagtcgcaagcatttcc 60
QY 65 qg-----gtgaatgagcagacagcagcagcagcagcagcagcagcagcagc 110
DB 61 gggcttccttcgcaattatgtagtgagcagcagcagcagcagcagcagcagcagc 120
QY 111 gtgagagataaacatgagcagcagcagcagcagcagcagcagcagcagcagcagc 170
DB 121 gtatgcaaaatctttacaaataaagcgttaataagcgttatattctctcgagaggaag--A 178
QY 171 cgaatcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 230
DB 179 ttatgctgctgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 238
QY 241 gggagagagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 290
DB 249 agcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 298
QY 291 cgaatcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 350
DB 299 cgaatcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 358
QY 351 gcaatcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 410
DB 359 gcaatcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 418
QY 411 atgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 470
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DB 1377 ggcgttcttcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1434
QY 1429 tgcgttaa 1434
DB 1435 tgcgttaa 1440

RESULT 12

US-08-632-470-36

; Sequence 36, Application US/08632470

; Patent No. 5976791

; GENERAL INFORMATION:

; APPLICANT: MABILAT, CLAUDE

; APPLICANT: RAULT, DIDIER

; TITLE OF INVENTION: NUCLEOTIDE FRAGMENTS CAPABLE OF

; HYBRIDIZING SPECIFICALLY TO PICKETT'SIA RNA OF PUNA AND

; TITLE OF INVENTION: HYBRIDIZING SPECIFICALLY TO PICKETT'SIA RNA OF PUNA AND

; TITLE OF INVENTION: THEIR USE AS PROBES OR PRIMERS

; NUMBER OF SEQUENCES: 53

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: OLIF & BERRIDGE

; STREET: P.O. BOX 19928

; CITY: ALEXANDRIA

; STATE: VA

; COUNTRY: USA

; ZIP: 22320

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/632,470

; FILING DATE: 08-JUL-1996

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: BERRIDGE, WILLIAM P

; REGISTRATION NUMBER: 30,024

; REFERENCE/DOCKET NUMBER: WPB 38238

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (703)-836-6400

; TELEFAX: (703)-836-2787

; INFORMATION FOR SEQ ID NO: 36:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1440 base pairs

; TYPE: nucleic acid

REGISTRATION NUMBER: 30,024
REFERENCE/PROJECT NUMBER: WPB 38238
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)-836-6400
TELEFAX: (703)-836-2787
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 1436 base pairs
TYPE: nuclear acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-632,470-34

Query Match 64.6%; Score 929; DB 2; Length 1436;
Best local similarity 80.7%; Pred. No. 3, 5, 6; 253;
Matches 1164; Conservative 0; Mismatches 29; Gaps 6;

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Search completed: February 26, 2002, 05:27:48
Job time: 12095 sec

RESULT	5
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LOCUS	
DEFINITION	AQ957272 DNA Atadiposis thaliana genomic clone LERA084, DNA
ACCESSION	AQ957272
VERSION	AQ957272.1
KEYWORDS	GSS,
SOURCE	t-hale class.

[illegible]

97 GTGGCTATGACACCGCTGCATGCTGTAGCTAACGGCTTTAAGTATCTGCTCTGGAGGATAC

826 gacgcgcgaagttaaaactcaaaqaatttaacnucac 862

37 GTTTCGCAAGATGAAACTCAAAAGTAATTCACGGGGGCT

	8
RESULTS	CNS10Q08 716 bp INA GSS 14-JUN-2001
Locus	Anopheles gambiae GSS SP6 end of clone Zep04 of NotI/HinfI I-
DEFINITION	from strain PEST of Anopheles gambiae (African malaria mosquito)
	genomic survey sequence.

	CNS01006	CNS01008	716 bp	INA	GSS	14-JUN-2001
LOCUS						
DEFINITION	Anopheles gambiae GSS SP6 end of clone ZAP04 of NotRedbel1 from strain PEST of Anopheles gambiae (African malaria mosquito) genomic survey sequence.					

ORGANISM	Anopheles gambiae
	Eukaryota; Metazoa; Arthropoda; Tracheata; Insecta;
	Pterygota; Neoptera; Endopterygota; Diptera; Nematocera;
	Culicoidae; Anophelinae.
REFERENCE	1 (bases 1 to 716)

REFERENCE
AUTHORS
TITLE
JOURNAL
1 (bases 1 to 716)
Genoscope.
Direct Submission
Submitted (16-FEB-2006) Genoscope - Centre National de Séquençage
BP 191 91006 EVRY cedex - FRANCE (E-mail : seq@genoscope.cns.fr)
- Web : www.genoscope.cns.fr

BP 191 91006. EVERY CEDEX: FRANCE (E-mail : scot@genoscope.cns.fr)
- Web : www.genoscope.cns.fr)

2 (bases 1 to 716)

Koth,C.W., Bray,F.T., KC,Z., Collins,F.H. and Weissenbach,J.
Direct Submission
Submitted (16-Feb-2000) RML, Institut Pasteur 25, rue du Dr

COMMENT
This clone is from an *A. quambae* BAC library provided by F. Collins and sequenced by genotype in collaboration with the Laboratory of Biochem. and Biol. Molec. of Ingels, Institut Roux, Paris 75015, France
Submitted (16-FEB-2000) BML, Institut Pasteur, 25, rue du Dr. Arce, 75013 Paris, France

FEATURES
source location/qualifiers
1. 716
/organism="Anopheles gambiae"
/strain="PEST"
/

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/return= "unpaired" space=
/strain="PES1"
/ab_str="favon.7165"
/cloname="26104"
/clone_lib="Not reName1"
/notes="end : Sp6"

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BASE COUNT	183 a	157 c	226 q	143 t	7 others
ORIGIN					
Querty Match:					
	27.9%	Score	400.8	DB	13; Length 716;

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Query Match: 27.9%; Score 400.8; DB 13; Length 716;
Best local Similarity 75.6%; Prod. No. 1.8e-89;
Matches 546; Conservative 5; Mismatch 103; 142; Indels 27; Gaps
0Y 159 qqdcaaaagccuacccctgtcgaaggacacacccatcagcttatcattcatt 2

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[illegible][illegible]

db 124 CTGACACACGGTCCACACTCCCTACCGAGACACACACAGTACGGGAATA TCAACAAATGAGAGG

Q7 339 aagcctatcacgaatgcgcctatctatcaaaactctctcgaatctatcaagcactttcc

db 184 AAG-CTGATGCACGCATGTCGGCTGTGTGTGACGAAGGCCCTTAGGTTGHAACAACTTCA-2

Dib 184 AAG-CTGATCAGACCATGCGGCTGCTGAGAGAGCCCTGAGCTGTGTAAGAGCACTTCA-4
QY 399 acgagagacgaatg-----atgacgctgacgctgagagagac-4
Dib 243 CCGAGGAGGAGAGGTGGTGAACTTAACTGCTTCATCAATTGAGCTACTACGCAAAAAAG-4

bb	243	CGGAGGAGGAAGGTGGTGAACCTAAATACGTTTCATCAATTGACGTTACCTCAGTAAAAAAGG
Qy	434	ccccgaactctctgcccacagccgcgqpalaaacaaagquqacclaaqcttactcgaat

Downloaded from <http://ajphaphysocpharm.sagepub.com/> at 11:01 11 November 2014

Suetterlin, R., Lin, X., Bai, G., Barstow, M., Roemer, C., Unterbach, T.,
 Goldblum, L., Liang, P., Crosby, T., and Fraser, C. M.
 A genome survey sequencing of landshark cecropia of
Marulius thaliana and identification of sequence-based
 polymorphisms
 (Unpublished, 2000)
 Contact: Xiaoying Lin
 The Institute for Genomic Research
 7712 Medical Center Dr., Rockville, MD 20850, USA
 Tel: 301 838 3200
 Fax: 301 838 3208
 Email: atliar@org
 For additional information, see <http://www.fishbase.org/databases.html>
 Similar to A. thaliana chloroplast sequence (CB:AP000423)
 Seq primer: 1R
 Class: shotgun.

Location/Qualifiers	1. 741	Score	DB 13	Length	741
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/strain "landberg erecta"		74.2%			
/date_xref "taxon:3705"		pred. No. 7.1e 89;			
/clone "LERA033"		0;	Mismatches 141;		
/clone_lib "LERA"					
/note "organ: leaf; Vector: pUC19; Total genomic DNA was sheared to 0.9-1 kbp before ligation."					
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ataacttaccaagcgcatgatcactagctgtcccagagatgatcagccacactggga 596
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qaqacacagccccaaactcctaacggagagagacgaatgggaatatlgacaataggcgc 338
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cagacacacggcccgagactctcaccggagagcagcagtgagggaattctccgcaatggcgca 536
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gaattgaagaagacacagcgaatgagaagacgcgaacatgaactgaatgaatgaatgaagc 696
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[illegible]

Sequence version 4.1
Copyright 1997-2000, Zymo Corporation, Ltd.

Maximum number of sequences: 1000

February 26, 2002, 09:38:36 Search time: 7100.49 seconds

(with 100 alignments)

334,784 Million cell updates/sec

Sequence version 4.1

February 26, 2002, 09:38:36 Search time: 7100.49 seconds

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334,784 Million cell updates/sec

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334,784 Million cell updates/sec

Sequence version 4.1

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334,784 Million cell updates/sec

Sequence version 4.1

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334,784 Million cell updates/sec

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334,784 Million cell updates/sec

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334,784 Million cell updates/sec

Sequence version 4.1

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(with 100 alignments)

334,784 Million cell updates/sec

Sequence version 4.1

February 26, 2002, 09:38:36 Search time: 7100.49 seconds

Result No.	Score	Match	Length	IP	IP	Accession
1	1298.4	90.4	1476	1	GT16SRNA	X80775.1
2	1296.8	90.3	1476	1	GT16SRNA	X80775.1
3	1295.2	90.2	1476	1	GT16SRNA	X80775.1
4	1294.4	90.0	1473	1	AB024492	AB024492.1
5	1278	89.0	1483	1	AB16SRNA	AB16SRNA.1
6	1277.6	89.0	1476	1	GT16SRNA	X80775.1
7	1274.8	88.6	1451	1	AB16SRNA	AB16SRNA.1
8	1272.8	88.6	1451	1	AB16SRNA	AB16SRNA.1
9	1266.4	87.5	1475	1	AB16SRNA	AB16SRNA.1
10	1265.4	87.3	1457	1	AB16SRNA	AB16SRNA.1
11	1259.4	87.3	1443	1	AB16SRNA	AB16SRNA.1
12	1251.2	87.1	1410	1	AB16SRNA	AB16SRNA.1
13	1250.6	87.1	1481	1	AB16SRNA	AB16SRNA.1
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16	1244.8	86.7	1451	1	AB024492	AB024492.1
17	1241	86.4	1481	1	AB16SRNA	AB16SRNA.1
18	1235.2	86.1	1453	1	AB024492	AB024492.1
19	1234.6	86.1	1481	1	AB024492	AB024492.1
20	1234.2	85.9	1443	1	AB024492	AB024492.1
21	1233.4	85.9	1481	1	AB16SRNA	AB16SRNA.1
22	1232.8	85.8	1411	1	AB024492	AB024492.1
23	1232.8	85.8	1411	1	AB024492	AB024492.1
24	1232.2	85.8	1411	1	AB024492	AB024492.1
25	1231.8	85.8	1411	1	AB024492	AB024492.1
26	1231.8	85.8	1475	1	AB024492	AB024492.1
27	1230.6	85.7	1411	1	AB024492	AB024492.1
28	1229	85.6	1411	1	AB024492	AB024492.1
29	1228.8	85.6	1482	1	AB16SRNA	AB16SRNA.1
30	1228.6	85.6	1443	1	AB024492	AB024492.1
31	1227.8	85.5	1454	1	AB024492	AB024492.1
32	1227.2	85.5	1480	1	AB024492	AB024492.1
33	1227	85.4	1483	1	AB16SRNA	AB16SRNA.1
34	1226.6	85.4	1483	1	AB16SRNA	AB16SRNA.1
35	1226.2	85.4	1498	1	AB024492	AB024492.1
36	1224.6	85.3	1426	1	AB16SRNA	AB16SRNA.1
37	1224.6	85.3	1483	1	AB16SRNA	AB16SRNA.1
38	1219	84.9	148	1	AB16SRNA	AB16SRNA.1
39	1215	84.6	1446	1	AB024492	AB024492.1
40	1214.6	84.6	1433	1	AB16SRNA	AB16SRNA.1
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42	1211	84.3	1443	1	AB16SRNA	AB16SRNA.1
43	1210	84.3	1409	1	AB16SRNA	AB16SRNA.1
44	1208.6	84.2	1428	1	AB16SRNA	AB16SRNA.1
45	1208.2	84.1	1490	1	AB16SRNA	AB16SRNA.1

ALIGNMENTS

Result	Score	Match	Length	IP	IP	Accession
GT16SRNA	1298.4	90.4	1476	1	GT16SRNA	X80775.1
DEFINITION	GT16SRNA	16S rRNA gene.				
ACCESSION	X80775					
VERSION	X80775.1	GT16SRNA				
KEYWORDS	16S ribosomal RNA; 16S rRNA gene.					
SOURCE	Glucobacter					
ORGANISM	Glucobacter					
REFERENCE	Bacterial Proteobacteria: alpha sub-class; Acetivibrio					
AUTHORS	1 (bases 1 to 1476)					
TITLE	Sievers, M.					
JOURNAL	Submitted (2000) M. Sievers, Food Microbiology, Swiss					
REFERENCE	2 (bases 1 to 1476)					
AUTHORS	Sievers, M., Gabor, C., Borsch, C., Luder, W., and Imber, M.					
TITLE	Phylogenetic position of Glucobacter species as a Glucobacter					

Note: No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed. It is derived by analysis of the total score distribution.

SUMMARY

Sequence version 4.1

[illegible][illegible]

DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	FEATURES	source
Acetobacter orleanensis gene for 16S ribosomal RNA, partial sequence.	AB032350	1	16S ribosomal RNA; 16S rRNA.	Acetobacter orleanensis (strain:IFO 14752) DNA.	Bacteria; Proteobacteria; alpha subdivision; Acetobacteraceae; Acetobacter.	1 (sites)	Lisdianti, P., Kawasaki, H., Yamada, Y., Seki, T., Uchimura, Y., and Komada, K.	Taxonomic study of the genus Acetobacter with descriptions of Acetobacter indonesiensis sp. nov., Acetobacter tropicalis sp. nov., Acetobacter estuensis (ex Carr 1958) nom. rev., Acetobacter orleanensis (ex Frateur 1950) nom. rev., Acetobacter orleanensis (ex Hunsicker 1956) nom. rev., and Acetobacter perolatus (ex Visser's Hoof 1925) nom. rev.	Unpublished (1999)	Location/Qualifiers	1..1443
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										/db_xref="taxon:104099"	
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										/product="16S ribosomal RNA"	
										..1443	
										/gene="16S rRNA"	
										342 a 326 c 476 g 299 t	
										BASE COUNT	
										ORIGIN	
										Query Match	86.98; Score 1248.6; DB 1; Length 1443;
										Best Local Similarity	93.38; Pred. No. 1; E: 0.0;
										Matches 1339; Conservative	0; Mismatches 89; Indels 7; Gaps 4;
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DB	67	67	67	67	67	67	67	67	67	67	67
QY	67	67	67	67	67	67	67	67	67	67	67
DB	67	67	67	67	67	67	67	67	67	67	67
QY	121	121	121	121	121	121	121	121	121	121	121
DB	127	127	127	127	127	127	127	127	127	127	127
QY	181	181	181	181	181	181	181	181	181	181	181
DB	187	187	187	187	187	187	187	187	187	187	187
QY	241	241	241	241	241	241	241	241	241	241	241
DB	247	247	247	247	247	247	247	247	247	247	247
QY	301	301	301	301	301	301	301	301	301	301	301
DB	307	307	307	307	307	307	307	307	307	307	307
QY	361	361	361	361	361	361	361	361	361	361	361
DB	367	367	367	367	367	367	367	367	367	367	367

RESULT 14

AB032350

LOCUS

AB032350 1443 bp DNA HCT 05-SEP-2000

XX claim 4; Page 16-17; 27pp; English.
 XX PS
 CC The present sequence represents the nucleotide sequence of the 16S rRNA
 CC gene of strain S877 (FERM ID-6752). This strain is a new microorganism
 CC belonging to the family Acetobacteraceae, and possibly belongs to a
 CC new genus analogous to the genus Acetobacter or the genus Gluconobacter.
 CC The specification also describes other new microorganisms belonging to
 CC the Acetobacteraceae family. The microorganism has the ability to produce
 CC xylitol or D-xylulose from glucose. The microorganisms were identified
 CC by collecting osmophilic microorganisms from soil, which were then
 CC examined for the ability to produce xylitol or D-xylulose from glucose.
 CC The new microorganisms may be used to industrially produce xylitol or
 CC D-xylulose from glucose by fermentation. The D-xylulose may be used
 CC for the production of xylitol, which is used as a sweetener in the food
 CC industry. In addition, xylitol may be used for fluid therapy in the
 CC treatment of diabetes. In addition, microorganisms of strain p528 may
 CC be used for production of ethanol.
 XX
 SO Sequence 1436 BP; 452 A; 319 C; 460 G; 305 T; 0 other;

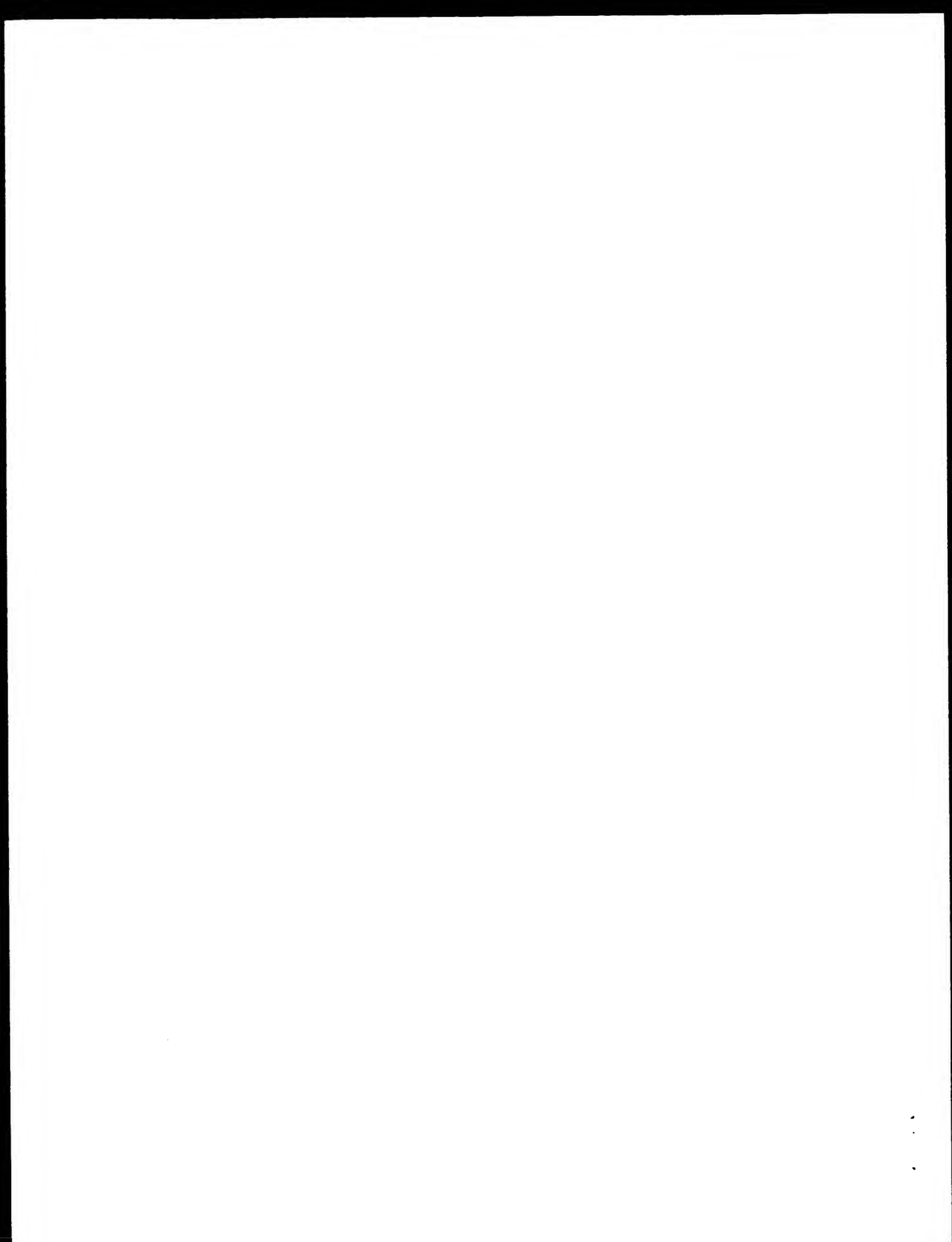
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 Mismatch 1436; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 QY 61 ttcgaagttaatgcagcaacgaatgaatgaacgttaagaacctatccagagtgaggata 120
 DB 61 ttcgaagttaatgcagcaacgaatgaatgaacgttaagaacctatccagagtgaggata 120
 QY 121 acacgcaggaacgtatgactacacgtatgactacacgtatgactacacgtatgactacacgt 180
 DB 121 acacgcaggaacgtatgactacacgtatgactacacgtatgactacacgtatgactacacgt 180
 QY 181 ttcgaagagcgtacgtttgatgaactatgattgaatgaatgaatgaatgaatgaatgaatgaat 240
 DB 181 ttcgaagagcgtacgtttgatgaactatgattgaatgaatgaatgaatgaatgaatgaatgaat 240
 QY 241 caatatactgcttgaagagagatgaacacacgtatgaacacacgtatgaacacacgtatgaacacac 300
 DB 241 caatatactgcttgaagagagatgaacacacgtatgaacacacgtatgaacacacgtatgaacacac 300
 QY 361 acggaagacacacgtacgagagatattggaacattggaacattggaacattggaacattggaacatt 420
 DB 361 acggaagacacacgtacgagagatattggaacattggaacattggaacattggaacattggaacatt 420
 QY 421 atagaaagaaac 480
 DB 421 atagaaagaaac 480
 QY 481 cgttgcctgcagatgaactgaag 540
 DB 481 cgttgcctgcagatgaactgaag 540
 QY 541 atccccac 600
 DB 541 atccccac 600
 QY 661 ttcgaag 660
 DB 661 ttcgaag 660
 QY 720 agggag 720
 DB 720 agggag 720

QY 721 taataacctgntagttccacagctatgaac 780
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 DB 791 ttcgaagtgcgaagcgttgaagcgttgaagcgttgaagcgttgaagcgttgaagcgttgaagcgttgaag 840
 QY 841 agcgaagcgttgaagcgttgaagcgttgaagcgttgaagcgttgaagcgttgaagcgttgaagcgttgaag 900
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 ID AAZ45682 standard: DNA; 1436 bp.
 AC AAZ45682;
 XX
 XX
 DT 06 APR 2000 (first entry)
 XX
 DE Nucleotide sequence of the 16S rRNA gene of strain p528.
 XX
 KW 16S rRNA gene; strain p528; FERM ID-6751; Acetobacteraceae; xylitol;
 RW D-xylulose, glucose, sweetener; fluid therapy; diabetes; ethanol; ss.
 XX
 OS Acetobacter sp.
 XX
 PN EP974646-A1.
 XX
 PD 26-JAN-2000.
 XX
 PF 07-JUL-1999; 99gp-0113149.
 XX
 PR 08-JUL-1998; 98jp-0194472.
 PP 30-OCT-1998; 98jp-0310398.

[illegible]



[illegible]

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1  RESULT 2
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3  ; Sequence 1, Application US/08276943
4  ; Patent No. 5607839
5  ; GENERAL INFORMATION:
6  ; APPLICANT: Tsubokura, Akira
7  ; APPLICANT: Yoneda, Hisashi
8  ; APPLICANT: Takaki, Mikihiro
9  ; APPLICANT: Kiyota, Takashi
10 ; APPLICANT: Kiyota, Takashi
11 ; TITLE OF INVENTION: BACTERIA BELONGING TO NEW GENUS AND
12 ; TITLE OF INVENTION: PROCESS FOR PRODUCTION OF CARBOHYDRATES USING SAME
13 ; NUMBER OF SEQUENCES: 1
14 ; CORRESPONDENCE ADDRESS:
15 ; ADDRESSEE: Seed & Perry
16 ; STREET: 6200 Columbia Center, 701 Fifth Avenue
17 ; CITY: Seattle
18 ; STATE: Washington
19 ; COUNTRY: USA
20 ; ZIP: 98104-7092
21 ; COMPUTER READABLE FORM:
22 ; MEDIUM TYPE: Floppy disk
23 ; COMPUTER: IBM PC compatible
24 ; OPERATING SYSTEM: PC DOS/MS DOS
25 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
26 ; CURRENT APPLICATION DATA:
27 ; APPLICATION NUMBER: US/08276943
28 ; FILING DATE: 19-01-1994
29 ; CLASSIFICATION: 435
30 ; ATTORNEY/AGENT INFORMATION:
31 ; NAME: Maki, David J
32 ; REGISTRATION NUMBER: 31,492
33 ; REFERENCE/DOCKET NUMBER: 700085.407
34 ; TELECOMMUNICATION INFORMATION:
35 ; TELEPHONE: (206) 622-4900
36 ; TELEFAX: (206) 682-6031
37 ; TELEX: 3723836 SEEDANBERRY
38 ; INFORMATION FOR SEQ ID NO: 1:
39 ; SEQUENCE CHARACTERISTICS:
40 ; LENGTH: 1452 base pairs
41 ; TYPE: nucleic acid
42 ; STRANDEDNESS: double
43 ; TOPOLOGY: linear
44 ; MOLECULE TYPE: cDNA to rRNA
45 ; US-08-276-943-1

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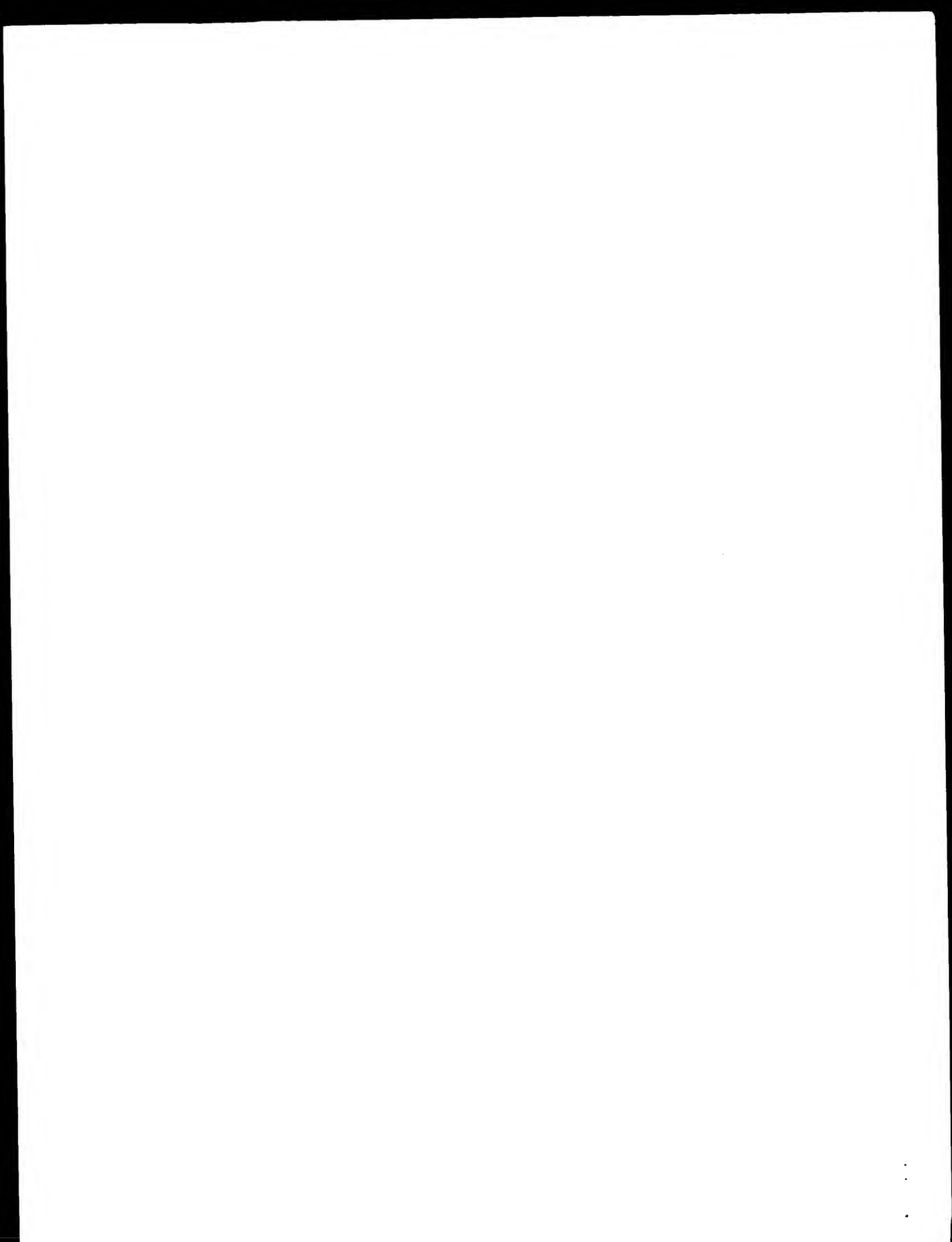
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RESULT 8
US-08-642-470-47
; Sequence 47, Application US-08-642470
; Patent No. 5976791
; GENERAL INFORMATION:
; APPLICANT: MARILYN, CLAUDE
; APPLICANT: RABBIT, DIDIER
; TITLE OF INVENTION: RECOMBINANT FRAGMENTS CAPABLE OF
; HYBRIDIZING WITH SEQUENCES OF DNA
; NUMBER OF INVENTIONS: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OLIEF & BERTRIDGE
; STREET: P.O. BOX 19928
; CITY: ALEXANDRIA
; STATE: VA
; COUNTRY: USA
; ZIP: 22304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patatol Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: 08-09-90, 470
; APPLICATION NUMBER: 08-09-90, 470
; FILING DATE: 08-JUL-1996
; CLASSIFICATION: 435
; AUTHORITY/AGENT INFORMATION:
; NAME: BERTRIDGE, WILLIAM P.
; REGISTRATION NUMBER: 30,024
; REFERENCE/AGENT NUMBER: 08-09-90, 470
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)-836-6400
; TELEFAX: (703)-836-2787
; INFORMATION FOR SEQ ID NO: 47:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1569 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: Linear
; MOLECULE TYPE: DNA (genomic)
US-08-642-470-47

Query Match: 64.8%; Score 940.4; Len 2; Length 1569;
Best Local Similarity 79.5%; Fred. No. 0;
Matches 1164; Conservative 0; Mismatches 266; Indels 34; Gaps 4;
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OPANI5W	Glucobacter corinus	Bacteria; Proteobacteria; alpha subphylum; Acetobacteraceae; Glucobacter
REFERENCE	1 (bases 1 to 1476)	
AUTHORS	Siewers, M.	
TITLE	Direct Submission	
JOURNAL	Submitted (23 AUG 1994) M. Siewers, Food Microbiology, Swiss Federal Inst. of Technology, ETH Zentrum, 1900, 8092 Zurich, SWITZERLAND	
REFERENCE	2 (bases 1 to 1476)	
AUTHORS	Siewers, M., Gaberthüel, C., Boesch, C., Ludwig, W. and Teuber, M.	
TITLE	Phylogenetic position of glucobacter species as a coherent cluster separated from all Acetobacter species on the basis of 16S ribosomal RNA sequences	
JOURNAL	16S Microbiol. Lett. 126 (2): 123-126 (1995)	
MEDLINE	95220639	
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07	301 acgagagagagatgagacatgagacatgagacatgagacatgagacat 360	
DB	306 acgagagagagatgagacatgagacatgagacatgagacatgagacat 365	
07	361 gtgtgtgaagagatgcttccgcttataaagccttccctacgaagatgatac 420	
DB	366 gtgtgtgaagagatgcttccgcttataaagccttccctacgaagatgatac 425	
07	421 ctgaagagagagatgagacatgagacatgagacatgagacatgagacat 480	
DB	426 cgttag 485	
07	481 cgttgcctgaagatgagacatgagacatgagacatgagacatgagacat 540	
DB	486 cgttgcctgaagatgagacatgagacatgagacatgagacatgagacat 545	
07	541 atcccgagagatgagacatgagacatgagacatgagacatgagacat 600	
DB	546 atcccgagagatgagacatgagacatgagacatgagacatgagacat 605	



Software version 4.5
Copyright (c) 1996-2000, Computer Ltd.

Randomly generated sequence using SW model

Run on: February 26, 2002, 05:40:33 : Search time 424.44 seconds

(without alignment)

1000, 45 hits, 45 updates/s

Hit list

Partial sequence

Alignment

Sequence

Score

Score

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Score

Score

Score

Score

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Score

Score

Score

Score

Score

Score

Score

Score

Score

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Score

Score

Score

Score

Score

Score

Score

Score

Score

Score

Score

Score

Score

Score

Score

Score

Score

Score

Score

Score

Score

Score

Score

Score

Score

Score

Score

Prod. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed.
Prod. No. is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	Description
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2	691	691	21	AAZ45685	Partial nucleotide
3	691	691	21	AAZ45686	Nucleotide sequence
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XX PS Claim 5; Page 17; 27pp; English.
XX
XX The present sequence represents a partial nucleotide sequence of the
CC 16S rRNA gene of strain S1019 (FERM BP-6754). This strain is a new
CC microorganism belonging to the family Acetobacteraceae, and possibly
CC belongs to a new genus analogous to the genus Acetobacter or the genus
CC Gluconobacter. The specification also describes other new microorganisms
CC belonging to the Acetobacteraceae family. The microorganism has the
CC ability to produce xylitol or D-xylulose from glucose; the microorganisms
CC were identified by collecting osmophilic microorganisms from soil, which
CC glucose, the new microorganisms may be used to industrially produce
CC xylitol or D-xylulose from glucose by fermentation. The D-xylulose may
CC be used for the production of xylitol, which is used as a sweetener in
CC the food industry. In addition, xylitol may be used for fluid therapy
CC in the treatment of diabetes. In addition, microorganisms of strain P528
CC may be used for production of ethanol.
XX
SQ Sequence 691 BP; 176 A; 142 C; 227 G; 146 T; 0 other;

Query Match 100.0%; Score 691; DB 21; Length 691;
Best Local Similarity 100.0%; Pred. No. 2,60-207;
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RESULT 2

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XX D-xylulose, glucose; sweetener; fluid therapy; diabetes; ethanol;
XX Acetobacter; Gluconobacter; ss.
XX
XX Unidentified.
XX
XX KP974646-A1.
XX
XX 26-JAN-2000.
XX
XX 07-JUL-1999; 99EP-0113149.
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XX 08-JUL-1998; 98JP-0194472.
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XX 30-OCT-1998; 98JP-0310398.
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XX 23 JAN 1999; 99JP-0012244.
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XX (AJIN ) AJINOMOTO KK.
XX
XX Mihata Y, Takeuchi S, Jojima Y, Iobuchi M, Endo K, Yokozeki K;
XX
XX WPI: 2000-100307/10.
XX
XX New microorganisms, useful for the production of D-xylulose or xylitol
XX
XX Claim 5; Page 18; 27pp; English.
XX
XX The present sequence represents a partial nucleotide sequence of the
CC 16S rRNA gene of strain S1019 (FERM BP-6754). This strain is a new
CC microorganism belonging to the family Acetobacteraceae, and possibly
CC belongs to a new genus analogous to the genus Acetobacter or the genus
CC Gluconobacter. The specification also describes other new microorganisms
CC belonging to the Acetobacteraceae family. The microorganism has the
CC ability to produce xylitol or D-xylulose from glucose. The microorganisms
CC were identified by collecting osmophilic microorganisms from soil, which
CC glucose, the new microorganisms may be used to industrially produce
CC xylitol or D-xylulose from glucose by fermentation. The D-xylulose may
CC be used for the production of xylitol, which is used as a sweetener in
CC the food industry. In addition, xylitol may be used for fluid therapy
CC in the treatment of diabetes. In addition, microorganisms of strain P528
CC may be used for production of ethanol.
XX
XX Sequence 691 BP; 176 A; 142 C; 227 G; 146 T; 0 other;
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Query Match 100.0%; Score 691; DB 21; Length 691;
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KW	D-xylose; glucose; sweetener; fluid therapy; diabetes; ethanol;	
KW	Acetobacter; Gluconobacter; SS.	
OS	Unidentified.	
XX		
PN	EP974646-AL.	
XX		
XX	26 JAN 2000.	
XX		
XX	07 JUL 1999; 99EP-0113449.	
XX		
PR	08 JUL 1998; 98JP-0194472.	
PR	30 OCT 1998; 98JP-0310398.	
XX	20 JAN 1999; 99JP-6012244.	
XX		
PA	(AJIN) AJIN-0610 KK.	
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XX	Mihara Y, Takeuchi S, Fujita Y, Tanuchi N, Yonezaki K;	
PT	WPT; 2000-108397/10.	
XX		
XX	New microorganisms, useful for the production of D-xylose or xyliol	
PT		
XX		
XX	Claim 5; Page 18; 27pp; English.	
XX		
CC	The present sequence represents a partial nucleotide sequence of the	
CC	16S rRNA gene of strain S1023 (PERM BP-6755). This strain is a new	
CC	microorganism belonging to the family Acetobacteraceae, and possibly	
CC	belongs to a new genus analogous to the genus Acetobacter or the genus	
CC	Gluconobacter. The specification also describes other new microorganisms	
CC	belonging to the Acetobacteraceae family. The microorganism has the	
CC	ability to produce xyliol or D xylose from glucose. The microorganisms	
CC	were identified by collecting osmophilic microorganisms from soil, which	
CC	were then examined for the ability to produce xyliol or D xylose from	
CC	glucose. The new microorganisms may be used to industrially produce	
CC	xyliol or D-xylose from glucose by fermentation. The D xylose may	
CC	be used for the production of xyliol, which is used as a sweetener in	
CC	the food industry. In addition, xyliol may be used for fluid therapy	
CC	in the treatment of diabetes. In addition, microorganisms of strain p528	
CC	may be used for production of ethanol.	
XX		
XX	Sequence 691 BP; 176 A; 142 C; 227 G; 146 T; 0 other.	

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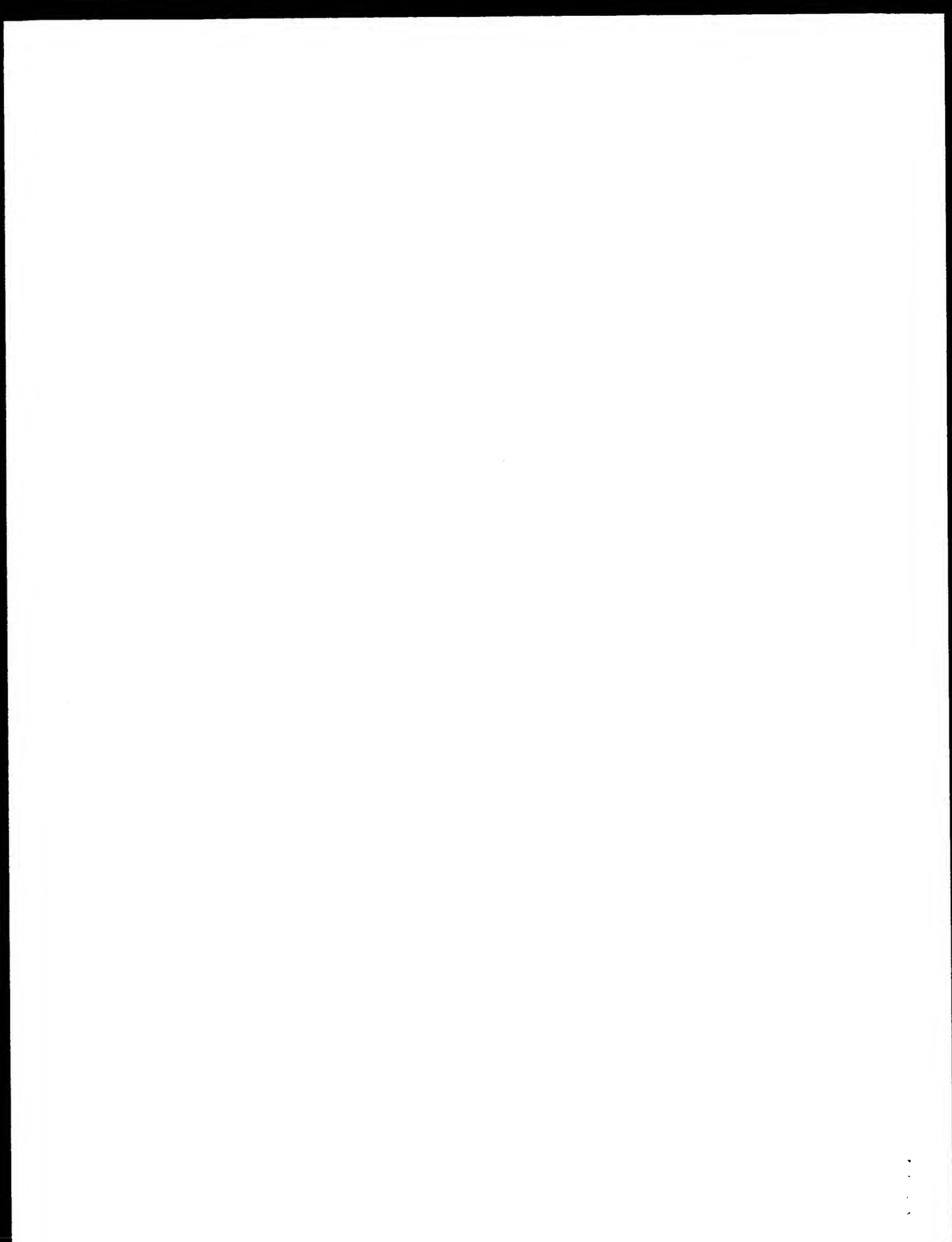
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LOCUS Acetobacter oxydans gene for 16S ribosomal RNA, partial
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 Acetobacter orleanensis
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 Acetobacter.
 1 (sites)
 Lisdianti,P., Kawasaki,H., Yamada,Y., Seki,T., Uchimura,Y., and
 Komada,K.
 Taxonomic study of the genus Acetobacter with descriptions of
 Acetobacter indonesiensis sp. nov., Acetobacter tropicalis sp.
 nov., Acetobacter estuensis (ex Carr 1969) nom. rev., Acetobacter
 loyensis (ex Frater 1960) nom. rev., Acetobacter orleanensis
 (ex Hennobert 1906) nom. rev., and Acetobacter peroxydans (ex
 Visser't Hooft 1925) nom. rev.
 Unpublished (1999)
 2 (bases 1 to 1443)
 Kawasaki,H. and Lisdianti,P.
 Direct Submission
 Submitted (10 SEP 1999) to the DDB/EMBL/GenBank database
 Kawasaki, The International Center for Biotechnology, Osaka
 University, 2-1, Yamada-oka, Suita, Osaka 565-0871, Japan
 (E-mail:kawasaki@osaka-u.ac.jp, tel:81-6-6879-7455,
 Fax:81-6-6879-7454)
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RESULT 4
AAZ45686
ID AAZ45686 standard; DNA; 691 bp.
XX
AC AAZ45686;
XX
DL 06-APR-2000 (first entry)
XX
DE Partial nucleotide sequence of the 16S rRNA gene of strain S1023.
XX
FW 16S rRNA gene; strain S1023; FERM 6755; Acetobacteraceae; xylitol;
KW D-xylose; glucose; fluid therapy; diabetes; ethanol;
KW Acetobacter; Gluconobacter; ss.
XX
OS Unidentified.
XX
PN EP974646-A1.
XX
PL 26-JAN-2000.
XX
PF 07-JUL-1999; 99EP-0113149.
XX
PR 08-JUL-1998; 98JP-0193472.
PR 30-OCT-1998; 98JP-0310398.
PR 20-JAN-1999; 99JP-0012244.
XX
EA (AJIN) AJINOMOTO KK.
XX
FI Mihara Y, Takeuchi S, Soejima T, Tanabe H, Endo K, Takeuchi K;
XX WPI; 2000-108397/10.
XX
DE New microorganisms, useful for the production of D-xylulose or xylitol.
XX
PL
PS Claim 5; Page 16; 27pp; English.
XX
XX
XX The present sequence represents a partial nucleotide sequence of the
XX 16S rRNA gene of strain S1023 (FERM 6755). This strain is a new
XX microorganism belonging to the family Acetobacteraceae, and possibly
XX belongs to a new genus analogous to the genus Acetobacter of the genus
XX Gluconobacter. The specification also describes other new microorganisms
XX belonging to the Acetobacteraceae family. The microorganism has the
XX ability to produce xylitol, D-xylulose, from glucose. The microorganisms
XX were identified by collecting osmophilic microorganisms from soil, which
XX were then examined for the ability to produce xylitol or D-xylulose from
XX glucose. The new microorganisms may be used to industrially produce
XX xylitol, D-xylulose, from glucose, fermentation. The D-xylulose may
XX be used for the production of xylitol, which is used as a sweetener in
XX the food industry. In addition, xylitol may be used for fluid therapy
XX in the treatment of diabetes. In addition, microorganisms of strain p528
XX may be used for production of ethanol.
XX
SQ Sequence 691 bp; 176 A; 142 C; 227 G; 146 T; 6 other.

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Query Match 99.1%; Score 684.6; DB 21; Length 691;
Best Local Similarity 99.4%; Pred. No. 2,70-295;
Matches 687; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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QY 1 tctgagagctgattgagagagctgattgagagagctgattgagagagctgattgag 120
DB 1 tctgagagctgattgagagagctgattgagagagctgattgagagagctgattgag 120
QY 121 acacacagagagagctgattgagagagctgattgagagagctgattgagagagct 180
DB 121 acacacagagagagctgattgagagagctgattgagagagctgattgagagagct 180

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QY 181 ttgagagagagctgattgagagagctgattgagagagctgattgagagagctgatt 240
DB 181 ttgagagagagctgattgagagagctgattgagagagctgattgagagagctgatt 240
QY 241 caatgagctgattgagagagagctgattgagagagctgattgagagagctgattgag 400
DB 241 caatgagctgattgagagagagctgattgagagagctgattgagagagctgattgag 400
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QY 361 gtagagagagagctgattgagagagctgattgagagagctgattgagagagctgattgag 420
DB 361 gtagagagagagctgattgagagagctgattgagagagctgattgagagagctgattgag 420
QY 421 ctgagagagagagagctgattgagagagctgattgagagagctgattgagagagctgatt 480
DB 421 ctgagagagagagagctgattgagagagctgattgagagagctgattgagagagctgatt 480
QY 481 gtagagagagagagctgattgagagagctgattgagagagctgattgagagagctgatt 540
DB 481 gtagagagagagagctgattgagagagctgattgagagagctgattgagagagctgatt 540
QY 541 atgagagagagagagctgattgagagagctgattgagagagctgattgagagagctgatt 600
DB 541 atgagagagagagagctgattgagagagctgattgagagagctgattgagagagctgatt 600
QY 601 ttagagagagagagagctgattgagagagctgattgagagagctgattgagagagctgatt 660
DB 601 ttagagagagagagagctgattgagagagctgattgagagagctgattgagagagctgatt 660
QY 661 agagagagagagagctgattgagagagctgattgagagagctgattgagagagctgatt 691
DB 661 agagagagagagagctgattgagagagctgattgagagagctgattgagagagctgatt 691

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RESULT 5

AAZ45682
ID AAZ45682 standard; DNA; 1438 bp.

XX AAZ45682;

XX 06-APR-2000 (first entry)

XX Nucleotide sequence of the 16S rRNA gene of strain p528.

XX 16S rRNA gene; strain p528; FERM 6755; Acetobacteraceae; xylitol;

XX D-xylulose; glucose; sweetener; fluid therapy; diabetes; ethanol; ss.

XX Acetobacter sp.

XX EP974646-A1.

XX 26-JAN-2000.

XX 07-JUL-1999; 99EP-0113149.

XX 08-JUL-1998; 98JP-0193472.

XX 30-OCT-1998; 98JP-0310398.

XX 20-JAN-1999; 99JP-0012244.

XX (AJIN) AJINOMOTO KK.

XX Mihara Y, Takeuchi S, Soejima T, Tanabe H, Endo K, Takeuchi K;

XX WPI; 2000-108397/10.

XX New microorganisms, useful for the production of D-xylulose or xylitol.

XX Claim 1; Page 15 16; 27pp; English.

XX

0Y 61 f f e q q q f f a a t a r e q a q q a t q a a l a a q q u t a r e a a c c t a t e c a g a q u t a g q a a l a 120
1b 1111111111 111111111111111111 11111111 11111111 11111111 11111111 11111111 11111111 126
0Y 67 f f e q q q a t a q e q q a q a q q q a t q a q a a g e q q a a t a t a q e e t f t a c t a c g a a l a 126
1b 1111111111 1111111111 11111111 11111111 11111111 11111111 11111111 11111111 11111111 11111111 126
0Y 121 a r e q q q a a a r e t q q q e t a a t a e c c a t a t a a c c t q a a q q t t a a a q e t t t t t t q e e t 180
1b 1111111111 1111111111 11111111 11111111 11111111 11111111 11111111 11111111 11111111 11111111 180
0Y 127 q e e e q a a a a r e t q q a t a a c c t a t a c q e e t t t q q q a a a q - - a t t a t e q q a 184
1b 1111111111 1111111111 11111111 11111111 11111111 11111111 11111111 11111111 11111111 11111111 184
0Y 181 f f a q a q q e e t a q t t a a t f a q e t a q t t q t t q q t a a a q a c t a c c a a q a c q a t 240
1b 1111111111 1111111111 11111111 11111111 11111111 11111111 11111111 11111111 11111111 11111111 240
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1b 1111111111 1111111111 11111111 11111111 11111111 11111111 11111111 11111111 11111111 11111111 244
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0Y 361 a t a t a q a a a a t e t e q a t t a t a a a c t t t a c t a q a a a t a t a c c t a c 420
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0Y 365 q t a q t a t a a a q e e t a a p t t a a a q t t t e a p t a a a a a a t a a t a a a t a a 424
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0Y 421 e t a 480
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0Y 481 e q t e q t e q a a t a q t a q a c t a a a a c c t a a c c t a a c c t t a t a c a t c a a t a t a a 540
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Job time: 12448 sec

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Comparison 100%

Maximum number of residues in the alignment 60

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Sequence alignment 60/60 (100%)
Maximum number of residues in the alignment 60

Sequence position 4, 5
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Sequence position 4, 5
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Maximum number of residues in the alignment 60

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Sequence alignment 60/60 (100%)
Maximum number of residues in the alignment 60

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Comparison 100%

Maximum number of residues in the alignment 60

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Sequence alignment 60/60 (100%)
Maximum number of residues in the alignment 60

Sequence position 4, 5
Comparison 100%

Maximum number of residues in the alignment 60

Pair 100% Identity 250/250 (100%)
Sequence alignment 60/60 (100%)
Maximum number of residues in the alignment 60

ALIGNMENTS

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US-09-902-693-4

Sequence 2
US-09-902-693-4

Sequence 3
US-09-902-693-4

Sequence 4
US-09-902-693-4

Sequence 5
US-09-902-693-4

Sequence 6
US-09-902-693-4

Sequence 7
US-09-902-693-4

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US-09-902-693-4

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Sequence 24
US-09-902-693-4

Sequence 25
US-09-902-693-4

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RESULT      2
US-09-902-694-4
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2  :
3  : GENERAL INFORMATION:
4  :
5  : APPLICANT: MIHARA, Yasuhiro
6  : APPLICANT: TAKEUCHI, Sonoko
7  : APPLICANT: JIJIIMA, Yasuko
8  : APPLICANT: TONOUCHI, Naoto
9  : APPLICANT: ICHIOJI, Ryoosuke
10 : APPLICANT: ICHIOJI, Ryoosuke
11 :
12 : TITLE OF INVENTION: N-VEL, MARGARETANUM AND METHOD FOR PRODUCING N-VELTOL OR
13 :
14 : TITLE OF INVENTION: N-VELTOL, N-XYLIDINSE
15 :
16 : FILE REFERENCE: 0010-1015-0
17 :
18 : CURRENT APPLICATION NUMBER: 09739792, 694
19 :
20 : PRIOR FILING DATE: 2001-07-12
21 : PRIOR APPLICATION NUMBER: 09/447,001
22 :
23 : PRIOR FILING DATE: 1999-07-02
24 : PRIOR APPLICATION NUMBER: JP 10-194472
25 :
26 : PRIOR FILING DATE: 1998-07-08
27 : PRIOR APPLICATION NUMBER: JP 10-316498
28 :
29 : PRIOR FILING DATE: 1998-10-30
30 : PRIOR APPLICATION NUMBER: JP 11-12244
31 :
32 : PRIOR FILING DATE: 1999-01-20
33 : NUMBER OF SEQ ID NOS: 5
34 :
35 : SOFTWARE: Patent In Ver., 2.1
36 :
37 : SEQ ID NO 4
38 :
39 : LENGTH: 691
40 :
41 : TYPE: DNA
42 :
43 : ORGANISM: Unknown organism
44 :
45 : FEATURE:
46 :
47 : OTHER INFORMATION: Description of Unknown organism: strain S1019
48 :
49 : US-09-902-694-4

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RESULT      3
US-09-902-693-2
; Sequence 2, Application US/09902694
; GENERAL INFORMATION:
; APPLICANT: MIHARA, Yasuhiro
; APPLICANT: TAKEUCHI, Sonoko
; APPLICANT: JOJIMA, Yasuko
; APPLICANT: TANOUCHI, Naoto
; APPLICANT: FUKUOKA, Ryosuke
; APPLICANT: TODOKI, Kenzo
; TITLE OF INVENTION: NOVEL MICROORGANISM A
; DATE OF INVENTION: D-XVLOJ05E
; FILE REFERENCE: 0010-1015-0
; CURRENT APPLICATION NUMBER: US/099402,693
; CURRENT FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: 094347,001
; PRIOR FILING DATE: 1999-07-02
; PRIOR APPLICATION NUMBER: JP 10-194472
; PRIOR FILING DATE: 1998-07-08

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Page 6

Page 6


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db 1345 gccccctgacgaaactgaacctca 1360
RESULT 13
US-09-897-516-3853
SEQUENCE 3853, Application US/09897516
GENERAL INFORMATION:
APPLICANT: Corbin, David R.
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Huesing, Joseph E.
APPLICANT: Krasomil, Esterfeld, Karina C.
APPLICANT: Malvar, Thomas M.
APPLICANT: Slater, Steven C.
APPLICANT: Spiridonov, Sergei
TITLE OF INVENTION: Xenorhabdus sp. Genome Sequences And Uses Thereof
FILE REFERENCE: 38-21(51847)B, 05/06/07, 516
CURRENT FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 60/215, 161
PRIOR FILING DATE: 2000-06-30
NUMBER OF SEQ ID NOS: 8409
SEQ ID NO 3853
LENGTH: 83080
TYPE: DNA
ORGANISM: Xenorhabdus sp.
FEATURE:
NAME/KEY: CDS
LOCATION: (1342)..(1466)
US-09-897-516-3853

Query Match 54.8%; Score 478.8; DB 6; Length 84080;
Best Local Similarity 74.6%; Pred. No. 1,9e+11;
Matches 549; Conservative 0; Mismatches 142; Indels 55; Gaps

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DB 1275 gaatgcgaacgtgaacgtttgaatgaatgaatgaatgaatgaacgtgaacgtgaacgt 1334
QY 666 gcaactgaacgtgaacgtgaacgtttgaatgaatgaatgaatgaatgaacgtgaacgt 691
DB 1335 gcaactgaacgtgaacgtgaacgtttgaatgaatgaatgaatgaatgaacgtgaacgt 691

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Database version: 4.5
Copyright (c) 1990-2000 Computer Ltd.

Multiple sequence search: 8348 seqs model

Run on: February 26, 2002, 05:25:25 : Search time: 7100.48 Seconds
(excluding alignment)

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Sequence: 111346 seqs, 624686756 residues

Sequence: 111346 seqs, 624686756 residues

Note: As the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and as determined by analysis of the total score distribution.

SUMMARY

Result No.	Score	Match	Length	DB	IL	Description
1	623.8	90.3	144	1	AB042351	AB042351 Acetobacter
2	619	89.6	147	1	AF127431	AF127431 Acetobacter
3	617	89.3	147	1	AF127432	AF127432 Acetobacter
4	612.6	88.7	147	1	AF127433	AF127433 Acetobacter
5	611	88.4	144	1	AB042350	AB042350 Acetobacter
6	611	88.4	147	1	AB042354	AB042354 Acetobacter
7	609.4	88.2	147	1	AF127434	AF127434 Acetobacter
8	607.8	88.0	147	1	AF127435	AF127435 Acetobacter
9	607.8	88.0	147	1	AF127436	AF127436 Acetobacter
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12	607.8	88.0	147	1	AF127439	AF127439 Acetobacter
13	607.8	88.0	147	1	AF127440	AF127440 Acetobacter
14	606.8	87.8	147	1	AF127441	AF127441 Acetobacter
15	606.8	87.8	147	1	AF127442	AF127442 Acetobacter
16	606.2	87.7	147	1	AF127443	AF127443 Acetobacter
17	606.2	87.7	147	1	AF127444	AF127444 Acetobacter
18	606	87.7	147	1	AF127445	AF127445 Acetobacter
19	605.8	87.7	147	1	AF127446	AF127446 Acetobacter
20	605.2	87.6	147	1	AF127447	AF127447 Acetobacter
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27	601.4	87.0	147	1	AF127454	AF127454 Acetobacter
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34	598.2	86.6	147	1	AF127461	AF127461 Acetobacter
35	597.8	86.5	147	1	AF127462	AF127462 Acetobacter
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44	592.8	85.8	147	1	AF127471	AF127471 Acetobacter
45	592.4	85.7	147	1	AF127472	AF127472 Acetobacter

ALIGNMENTS

Result No.	Score	Match	Length	DB	IL	Description
1	623.8	90.3	144	1	AB042351	AB042351 Acetobacter
2	619	89.6	147	1	AF127431	AF127431 Acetobacter
3	617	89.3	147	1	AF127432	AF127432 Acetobacter
4	612.6	88.7	147	1	AF127433	AF127433 Acetobacter
5	611	88.4	144	1	AB042350	AB042350 Acetobacter
6	611	88.4	147	1	AB042354	AB042354 Acetobacter
7	609.4	88.2	147	1	AF127434	AF127434 Acetobacter
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18	606	87.7	147	1	AF127445	AF127445 Acetobacter
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20	605.2	87.6	147	1	AF127447	AF127447 Acetobacter
21	604.6	87.5	147	1	AF127448	AF127448 Acetobacter
22	604.6	87.5	147	1	AF127449	AF127449 Acetobacter
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38	597	86.4	147	1	AF127465	AF127465 Acetobacter
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44	592.8	85.8	147	1	AF127471	AF127471 Acetobacter
45	592.4	85.7	147	1	AF127472	AF127472 Acetobacter

AB042351 Acetobacter
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Version					
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Source					
Acetobacter orlenensis					
Bacteria; Proteobacteria; alpha subdivision; Acetobacteraceae;					
Acetobacter.					
Reference					
Lisdianty L.P., Kawasaki M., Yamada Y., Sasaki J., Uchimura Y., and Komagata K.					
Title					
Taxonomic study of the genus Acetobacter with descriptions of Acetobacter indonesiensis sp. nov., Acetobacter tropicalis sp. nov., Acetobacter orlenensis (ex cat. 1958) nom. rev., Acetobacter javanensis (ex Frauer 1960) nom. rev., Acetobacter orlenensis (ex Henneberg 1906) nom. rev., and Acetobacter periphrasus (ex Visser et Boett 1925) nom. rev.					
Journal					
unpublished (1999)					
Authors					
Kawasaki M. and Lisdianty L.P.					
Title					
Direct Submission					
Journal					
Submitted to Seq. 1999 by the Faculty of Biotechnology, Osaka University, 2-1, Yamadaoka, Suita, Osaka 565-0871 Japan (E-mail:kawasaki@biotech.osaka-u.ac.jp, Tel:81-6-6879-7455, Fax:81-6-6879-7454) Location/Qualifiers 1..1443 /organism "Acetobacter orlenensis" /strain "IFO 14752" /db_xref="taxon:104099" c1..>1443 /gene "16S rRNA" /product="16S ribosomal RNA" 1..1443 /gene:"16S rRNA" 342 a 326 c 476 g 299 t					
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ORIGIN					
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DB	127	ACTCGCGGAACCTGGAGCTAAATACGATGATGAAGCTTAACATGAGCTTAACAGGCTGAGCT	186		
QY	181	TAGGAAGAGCTGCCTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	240		
DB	187	GTCGAGAGGCTGGGCTTTGATAGCTTTCTGTGGGGGTAAATGAGCTACCAAGAGGATGAT	246		
QY	241	CATATCTGATTTGAGGATGATCAAGCAAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCT	300		
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QY	301	ACGAGAGCAACATGAGGATGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGAT	360		
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QY	361	GTGTCGAGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGAT	420		
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[illegible]

REF ID	Accession	Species	Gene	Length	GC	Notes
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3	AF011113	<i>Escherichia coli</i>	16S rRNA	1641	50.8	
4	AF011114	<i>Escherichia coli</i>	16S rRNA	1641	50.8	
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6	AF011116	<i>Escherichia coli</i>	16S rRNA	1641	50.8	
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8	AF011118	<i>Escherichia coli</i>	16S rRNA	1641	50.8	
9	AF011119	<i>Escherichia coli</i>	16S rRNA	1641	50.8	
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14	AF011124	<i>Escherichia coli</i>	16S rRNA	1641	50.8	
15	AF011125	<i>Escherichia coli</i>	16S rRNA	1641	50.8	
16	AF011126	<i>Escherichia coli</i>	16S rRNA	1641	50.8	
17	AF011127	<i>Escherichia coli</i>	16S rRNA	1641	50.8	
18	AF011128	<i>Escherichia coli</i>	16S rRNA	1641	50.8	
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27 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000 1001 1002 1003 1004 1005 1006 1007 1008 1009 1010 1011 1012 1013 1014 1015 1016 1017 1018 1019 1020 1021 1022 1023 1024 1025 1026 1027 1028 1029 1030 1031 1032 1033 1034 1035 1036 1037 1038 1039 1040 1041 1042 1043 1044 1045 1046 1047 1048 1049 1050 1051 1052 1053 1054 1055 1056 1057 1058 1059 1060 1061 1062 1063 1064 1065 1066 1067 1068 1069 1070 1071 1072 1073 1074 1075 1076 1077 1078 1079 1080 1081 1082 1083 1084 1085 1086 1087 1088 1089 1090 1091 1092 1093 1094 1095 1096 1097 1098 1099 1100 1101 1102 1103 1104 1105 1106 1107 1108 1109 1110 1111 1112 1113 1114 1115 1116 1117 1118 1119 1120 1121 1122 1123 1124 1125 1126 1127 1128 1129 1130 1131 1132 1133 1134 1135 1136 1137 1138 1139 1140 1141 1142 1143 1144 1145 1146 1147 1148 1149 1150 1151 1152 1153 1154 1155 1156 1157 1158 1159 1160 1161 1162 1163 1164 1165 1166 1167 1168 1169 1170 1171 1172 1173 1174 1175 1176 1177 1178 1179 1180 1181 1182 1183 1184 1185 1186 1187 1188 1189 1190 1191 1192 1193 1194 1195 1196 1197 1198 1199 1200 1201 1202 1203 1204 1205 1206 1207 1208 1209 1210 1211 1212 1213 1214 1215 1216 1217 1218 1219 1220 1221 1222 1223 1224 1225 1226 1227 1228 1229 1230 1231 1232 1233 1234 1235 1236 1237 1238 1239 1240 1241 1242 1243 1244 1245 1246 1247 1248 1249 1250 1251 1252 1253 1254 1255 1256 1257 1258 1259 1260 1261 1262 1263 1264 1265 1266 1267 1268 1269 1270 1271 1272 1273 1274 1275 1276 1277 1278 1279 1280 1281 1282 1283 1284 1285 1286 1287 1288 1289 1290 1291 1292 1293 1294 1295 1296 1297 1298 1299 1300 1301 1302 1303 1304 1305 1306 1307 1308 1309 1310 1311 1312 1313 1314 1315 1316 1317 1318 1319 1320 1321 1322 1323 1324 1325 1326 1327 1328 1329 1330 1331 1332 1333 1334 1335 1336 1337 1338 1339 1340 1341 1342 1343 1344 1345 1346 1347 1348 1349 1350 1351 1352 1353 1354 1355 1356 1357 1358 1359 1360 1361 1362 1363 1364 1365 1366 1367 1368 1369 1370 1371 1372 1373 1374 1375 1376 1377 1378 1379 1380 1381 1382 1383 1384 1385 1386 1387 1388 1389 1390 1391 1392 1393 1394 1395 1396 1397 1398 1399 1400 1401 1402 1403 1404 1405 1406 1407 1408 1409 1410 1411 1412 1413 1414 1415 1416 1417 1418 1419 1420 1421 1422 1423 1424 1425 1426 1427 1428 1429 1430 1431 1432 1433 1434 1435 1436 1437 1438 1439 1440 1441 1442 1443 1444 1445 1446 1447 1448 1449 1450 1451 1452 1453 1454 1455 1456 1457 1458 1459 1460 1461 1462 1463 1464 1465 1466 1467 1468 1469 1470 1471 1472 1473 1474 1475 1476 1477 1478 1479 1480 1481 1482 1483 1484 1485 1486 1487 1488 1489 1490 1491 1492 1493 1494 1495 1496 1497 1498 1499 1500 1501 1502 1503 1504 1505 1506 1507 1508 1509 1510 1511 1512 1513 1514 1515 1516 1517 1518 1519 1520 1521 1522 1523 1524 1525 1526 1527 1528 1529 1530 1531 1532 1533 1534 1535 1536 1537 1538 1539 1540 1541 1542 1543 1544 1545 1546 1547 1548 1549 1550 1551 1552 1553 1554 1555 1556 1557 1558 1559 1560 1561 1562 1563 1564 1565 1566 1567 1568 1569 1570 1571 1572 1573 1574 1575 1576 1577 1578 1579 1580 1581 1582 1583 1584 1585 1586 1587 1588 1589 1590 1591 1592 1593 1594 1595 1596 1597 1598 1599 1600 1601 1602 1603 1604 1605 1606 1607 1608 1609 1610 1611 1612 1613 1614 1615 1616 1617 1618 1619 1620 1621 1622 1623 1624 1625 1626 1627 1628 1629 1630 1631 1632 1633 1634 1635 1636 1637 1638 1639 1640 1641 1642 1643 1644 1645 1646 1647 1648 1649 1650 1651 1652 1653 1654 1655 1656 1657 1658 1659 1660 1661 1662 1663 1664 1665 1666 1667 1668 1669 1670 1671 1672 1673 1674 1675 1676 1677 1678 1679 1680 1681 1682 1683 1684 1685 1686 1687 1688 1689 1690 1691 1692 1693 1694 1695 1696 1697 1698 1699 1700 1701 1702 1703 1704 1705 1706 1707 1708 1709 1710 1711 1712 1713 1714 1715 1716 1717 1718 1719 1720 1721 1722 1723 1724 1725 1726 1727 1728 1729 1730 1731 1732 1733 1734 1735 1736 1737 1738 1739 1740 1741 1742 1743 1744 1745 1746 1747 1748 1749 1750 1751 1752 1753 1754 1755 1756 1757 1758 1759 1760 1761 1762 1763 1764 1765 1766 1767 1768 1769 1770 1771 1772 1773 1774 1775 1776 1777 1778 1779 1780 1781 1782 1783 1784 1785 1786 1787 1788 1789 1790 1791 1792 1793 1794 1795 1796 1797 1798 1799 1800 1801 1802 1803 1804 1805 1806 1807 1808 1809 1810 1811 1812 1813 1814 1815 1816 1817 1818 1819 1820 1821 1822 1823 1824 1825 1826 1827 1828 1829 1830 1831 1832 1833 1834 1835 1836 1837 1838 1839 1840 1841 1842 1843 1844 1845 1846 1847 1848 1849 1850 1851 1852 1853 1854 1855 1856 1857 1858 1859 1860 1861 1862 1863 1864 1865 1866 1867 1868 1869 1870 1871 1872 1873 1874 1875 1876 1877 1878 1879 1880 1881 1882 1883 1884 1885 1886 1887 1888 1889 1890 1891 1892 1893 1894 1895 1896 1897 1898 1899 1900 1901 1902 1903 1904 1905 1906 1907 1908 1909 1910 1911 1912 1913 1914 1915 1916 1917 1918 1919 1920 1921 1922 1923 1924 1925 1926 1927 1928 1929 1930 1931 1932 1933 1934 1935 1936 1937 1938 1939 1940 1941 1942 1943 1944 1945 1946 1947 1948 1949 1950 1951 1952 1953 1954 1955 1956 1957 1958 1959 1960 1961 1962 1963 1964 1965 1966 1967 1968 1969 1970 1971 1972 1973 1974 1975 1976 1977 1978 1979 1980 1981 1982 1983 1984 1985 1986 1987 1988 1989 1990 1991 1992 1993 1994 1995 1996 1997 1998 1999 2000 2001 2002 2003 2004 2005 2006 2007 2008 2009 2010 2011 2012 2013 2014 2015 2016 2017 2018 2019 2020 2021 2022 2023 2024 2025 2026 2027 2028 2029 2030 2031 2032 2033 2034 2035 2036 2037 2038 2039 2040 2041 2042 2043 2044 2045 2046 2047 2048 2049 2050 2051 2052 2053 2054 2055 2056 2057 2058 2059 2060 2061 2062 2063 2064 2065 2066 2067 2068 2069 2070 2071 2072 2073 2074 2075 2076 2077 2078 2079 2080 2081 2082 2083 2084 2085 2086 2087 2088 2089 2090 2091 2092 2093 2094 2095 2096 2097 2098 2099 2100 2101 2102 2103 2104 2105 2106 2107 2108 2109 2110 2111 2112 2113 2114 2115 2116 2117 2118 2119 2120 2121 2122 2123 2124 2125 2126 2127 2128 2129 2130 2131 2132 2133 2134 2135 2136 2137 2138 2139 2140 2141 2142 2143 2144 2145 2146 2147 2148 2149 2150 2151 2152 2153 2154 2155 2156 2157 2158 2159 2160 2161 2162 2163 2164 2165 2166 2167 2168 2169 2170 2171 2172 2173 2174 2175 2176 2177 2178 2179 2180 2181 2182 2183 2184 2185 2186 2187 2188 2189 2190 2191 2192 2193 2194 2195 2196 2197 2198 2199 2200 2201 2202 2203 2204 2205 2206 2207 2208 2209 2210 2211 2212 2213 2214 2215 2216 2217 2218 2219 2220 2221 2222 2223 2224 2225 2226 2227 2228 2229 2230 2231 2232 2233 2234 2235 2236 2237 2238 2239 2240 2241 2242 2243 2244 2245 2246 2247 2248 2249 2250 2251 2252 2253 2254 2255 2256 2257 2258 2259 2260 2261 2262 2263 2264 2265 2266 2267 2268 2269 2270 2271 2272 2273 2274 2275 2276 2277 2278 2279 2280 2281 2282 2283 2284 2285 2286 2287 2288 2289 2290 2291 2292 2293 2294 2295 2296 2297 2298 2299 2300 2301 2302 2303 2304 2305 2306 2307 2308 2309 2310 2311 2312 2313 2314 2315 2316 2317 2318 2319 2320 2321 2322 2323 2324 2325 2326 2327 2328 2329 2330 2331 2332 2333 2334 2335 2336 2337 2338 2339 2340 2341 2342 2343 2344 2345 2346 2347 2348 2349 2350 2351 2352 2353 2354 2355 2356 2357 2358 2359 2360 2361 2362 2363 2364 2365 2366 2367 2368 2369 2370 2371 2372 2373 2374 2375 2376 2377 2378 2379 2380 2381 2382 2383 2384 2385 2386 2387 2388 2389 2390 2391 2392 2393 2394 2395 2396 2397 2398 2399 2400 2401 2402 2403 2404 2405 2406 2407 2408 2409 2410 2411 2412 2413 2414 2415 2416 2417 2418 2419 2420 2421 2422 2423 2424 2425 2426 2427 2428 2429 2430 2431 2432 2433 2434 2435 2436 2437 2438 2439 2440 2441 2442 2443 2444 2445 2446 2447 2448 2449 2450 2451 2452 2453 2454 2455 2456 2457 2458 2459 2460 2461 2462 2463 2464 2465 2466 2467 2468 2469 2470 2471 2472 2473 2474 2475 2476 2477 2478 2479 2480 2481 2482 2483 2484 2485 2486 2487 2488 2489 2490 2491 2492 2493 2494 2495 2496 2497 2498 2499 2500 2501 2502 2503 2504 2505 2506 2507 2508 2509 2510 2511 2512 2513 2514 2515 2516 2517 2518 2519 2520 2521 2522 2523 2524 2525 2526 2527 2528 2529 2530 2531 2532 2533 2534 2535 2536 2537 2538 2539 2540 2541 2542 2543 2544 2545 2546 2547 2548 2549 2550 2551 2552 2553 2554 2555 2556 2557 2558 2559 2560 2561 2562 2563 2564 2565 2566 2567 2568 2569 2570 2571 2572 2573 2574 2575 2576 2577 2578 2579 2580 2581 2582 2583 2584 2585 2586 2587 2588 2589 2590 2591 2592 2593 2594 2595 2596 2597 2598 2599 2600 2601 2602 2603 2604 2605 2606 2607 2608 2609 2610 2611 2612 2613 2614 2615 2616 2617 2618 2619 2620 2621 2622 2623 2624 2625 2626 2627 2628 2629 2630 2631 2632 2633 2634 2635 2636 2637 2638 2639 2640 2641 2642 2643 2644 2645 2646 2647 2648 2649 2650 2651 2652 2653 2654 2655 2656 2657 2658 2659 2660 2661 2662 2663 2664 2665 2666 2667 2668 2669 2670 2671 2672 2673 2674 2675 2676 2677 2678 2679 2680 2681 2682 2683 2684 2685 2686 2687 2688 2689 2690 2691 2692 2693 2694 2695 2696 2697 2698 2699 2700 2701 2702 2703 2704 2705 2706 2707 2708 2709 2710 2711 2712 2713 2714 2715 2716 2717 2718 2719 2720 2721 2722 2723 2724 2725 2726 2727 2728 2729 2730 2731 2732 2733 2734 2735 2736 2737 2738 2739 2740 2741 2742 2743 2744 2745 2746 2747 2748 2749 2750 2751 2752 2753 2754 2755 2756 2757 2758 2759 2760 2761 2762 2763 2764 2765 2766 2767 2768 2769 2770 2771 2772 2773 2774 2775 2776 
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The present sequence represents the nucleotide sequence of the 16S rRNA gene of strain p29 (FPM 46-93). This strain is a new microorganism belonging to the family Acetivibrionaceae. The classification of also described other new microorganisms belonging to this family. The microorganism has the ability to produce xylitol or α -xylofuranose from glucose. The microorganisms were identified by collected osmophilic *acetivibrionaceae* from soil to which were then examined for the ability to produce xylitol or α -xylofuranose from glucose. The new microorganisms may be used to industrially produce xylitol or α -xylofuranose from glucose by fermenting the α -xylofuranose may be used in the production of xylitol, which is used as a sweetener in the food industry. In addition, xylitol may be used for clinical therapy in the treatment of diabetics. In addition, new microorganisms strain p29 may be used for production of ethanol.

$\mathcal{F}_1 = \{f_1, f_2, f_3, f_4, f_5, f_6, f_7, f_8, f_9, f_{10}, f_{11}, f_{12}, f_{13}, f_{14}, f_{15}, f_{16}, f_{17}, f_{18}, f_{19}, f_{20}, f_{21}, f_{22}, f_{23}, f_{24}, f_{25}, f_{26}, f_{27}, f_{28}, f_{29}, f_{30}, f_{31}, f_{32}, f_{33}, f_{34}, f_{35}, f_{36}, f_{37}, f_{38}, f_{39}, f_{40}, f_{41}, f_{42}, f_{43}, f_{44}, f_{45}, f_{46}, f_{47}, f_{48}, f_{49}, f_{50}, f_{51}, f_{52}, f_{53}, f_{54}, f_{55}, f_{56}, f_{57}, f_{58}, f_{59}, f_{60}, f_{61}, f_{62}, f_{63}, f_{64}, f_{65}, f_{66}, f_{67}, f_{68}, f_{69}, f_{70}, f_{71}, f_{72}, f_{73}, f_{74}, f_{75}, f_{76}, f_{77}, f_{78}, f_{79}, f_{80}, f_{81}, f_{82}, f_{83}, f_{84}, f_{85}, f_{86}, f_{87}, f_{88}, f_{89}, f_{90}, f_{91}, f_{92}, f_{93}, f_{94}, f_{95}, f_{96}, f_{97}, f_{98}, f_{99}, f_{100}\}$

Category	Match	800,000	Score	600,000	DB	21	Length	1438
Test	Test	92.6 <td>Prod.</td> <td>No.</td> <td>1,900,000 <td></td> <td></td> <td></td> </td>	Prod.	No.	1,900,000 <td></td> <td></td> <td></td>			
Matches	600,000	Mismatch	600,000	Mismatch	600,000			

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XX	AAH49546;
XX	AC
XX	24-SEP-2001 (first entry)
XX	UU
XX	Arrobacterium stellulatum DNA sequence #1.
DE	
XX	Carbohydrase; food industry; ds.
KW	
XX	Arrobacterium stellulatum.
US	
XX	JF2001146961 A.
XX	
XX	22 MAY 2001.
PP	
XX	18-NOV-1999; 96JP-0x28167.
PF	
XX	18 NOV 1999; 96JP-0x28167.
PR	
XX	(KAY : KAY) EMBL500152; EMBL500153.
PA	
XX	WI, 2001 460259/50.
PK	
XX	Improving carbohydrase producing ability of bacteria in food industry,
PT	
XX	involves cultivating bacteria having carbohydrase producing ability in
PT	
XX	presence of bacteria without carbohydrase producing ability .
PI	
XX	bislosure; Page 7; 12pp; Japanese.
PS	
XX	The present invention relates to a method for improving carbohydrase
CC	
CC	producing ability of bacteria, the method involves cultivating bacteria
CC	having carbohydrase producing ability in the presence of bacteria or in a
CC	culture without carbohydrase producing ability, the bacteria with
CC	improved carbohydrase producing ability are useful in the food industry.
CC	The present sequence from Arrobacterium stellulatum was used to
CC	illustrate the present method.
XX	
XX	Sequence 1405 BP; 437 A; 433 C; 454 G; 261 T; no other;
SO	

Query Match 74.0%; Success 511; 148.22; Length 34.01;
best local Similarity 85.76%; Prec. No. 4,600.10;
Matches 580; Conservatives 0; Mismatches 95; Models 1;
100% 1;

[illegible]

RESULT 15
US-08-632-470-44
; Sequence 44, Application US/09612170
; Patent No. 5976791
; GENERAL INFORMATION:
; APPLICANT: MABTAT, CLAUDE
; APPLICANT: MABTAT, CLAUDE

RESULT 14
 1 US 08-6,42-470 29
 2 Sequence 29, Application US/08632470
 3 Patent No. 5976791
 4
 5 GENERAL INFORMATION:
 6
 7 APPLICANT: MAHLAT, CLAUDE
 8
 9 APPLICANT: MAHLAT, DIDIER
 10
 11 TITLE OF INVENTOR: NUCLEOTIDE FRAGMENTS CAPABLE OF
 12
 13 TITLE OF INVENTOR: HYBRIDIZING SPECIFICALLY TO ERYTHROCYTA PURA OR PUNA AND
 14
 15 TITLE OF INVENTOR: THEIR USE AS PROBES OR PRIMERS
 16
 17 NUMBER OF SEQUENCES: 53
 18
 19 CORRESPONDENCE ADDRESS:
 20
 21 ADDRESSEE: OLITE & BERTHOGE
 22
 23 STREET: P.O. BOX 19246
 24
 25 CITY: ALEXANDRIA
 26
 27 STATE: VA
 28
 29 COUNTRY: USA
 30
 31 ZIP: 22420
 32
 33 COMPUTER READABLE FORM:
 34
 35 HIGH TYPE: Flatfile disk
 36
 37 COMPUTER: IBM PC compatible
 38
 39 OPERATING SYSTEM: DOS/MS-DOS
 40
 41 SOFTWARE: Patent In Release #1.0, Version #1.40
 42
 43 CURRENT APPLICATION DATA:
 44
 45 APPLICATION NUMBER: 08/086,42-470
 46
 47 FILING DATE: 08 JUL 1996
 48
 49 CLASSIFICATION: 43
 50
 51 ATTORNEY/AGENT INFORMATION:
 52
 53 NAME: BERTHOGE, WILLIAM F
 54
 55 REGISTRATION NUMBER: 40,024
 56
 57 REFERENCE/INCKET NUMBER: WFO 19248

